

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: O'Brien, John S.
Kishimoto, Yasuo

(ii) TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Knobbe, Martens, Olson and Bear
- (B) STREET: 620 Newport Center Drive, Sixteenth Floor
- (C) CITY: Newport Beach
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 92660

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/484,594
- (B) FILING DATE: 07-JUN-1995
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/100,247
- (B) FILING DATE: 30-JUL-1993

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Israelsen, Ned A
- (B) REGISTRATION NUMBER: 29,655
- (C) REFERENCE/DOCKET NUMBER: MYELOS.002DV2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619-235-8550
- (B) TELEFAX: 619-235-0176
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
1 5 10 15
Thr Glu Lys Glu Ile Leu
20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1 5 10 15
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
20 25 30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
35 40 45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
50 55 60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65 70 75 80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
85 90 95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
100 105 110
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
115 120 125
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
130 135 140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
145 150 155 160
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
165 170 175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
180 185 190
Asp Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile Gln

		195					200				205								
Thr	Ala	Val	Arg	Thr	Asn	Ser	Thr	Phe	Val	Gln	Ala	Leu	Val	Glu	His				
	210					215					220								
Val	Lys	Glu	Glu	Cys	Asp	Arg	Leu	Gly	Pro	Gly	Met	Ala	Asp	Ile	Cys				
225					230					235					240				
Lys	Asn	Tyr	Ile	Ser	Gln	Tyr	Ser	Glu	Ile	Ala	Ile	Gln	Met	Met	Met				
				245				250						255					
His	Met	Gln	Pro	Lys	Glu	Ile	Cys	Ala	Leu	Val	Gly	Phe	Cys	Asp	Glu				
		260					265						270						
Val	Lys	Glu	Met	Pro	Met	Gln	Thr	Leu	Val	Pro	Ala	Lys	Val	Ala	Ser				
	275						280					285							
Lys	Asn	Val	Ile	Pro	Ala	Leu	Asp	Leu	Val	Asp	Pro	Ile	Lys	Lys	His				
	290					295					300								
Glu	Val	Pro	Ala	Lys	Ser	Asp	Val	Tyr	Cys	Glu	Val	Cys	Glu	Phe	Leu				
305					310					315					320				
Val	Lys	Glu	Val	Thr	Lys	Leu	Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu				
				325				330						335					
Ile	Leu	Asp	Ala	Phe	Asp	Lys	Met	Cys	Ser	Lys	Leu	Pro	Lys	Ser	Leu				
			340				345						350						
Ser	Glu	Glu	Cys	Gln	Glu	Val	Val	Asp	Thr	Tyr	Gly	Ser	Ser	Ile	Leu				
	355					360						365							
Ser	Ile	Leu	Leu	Glu	Glu	Val	Ser	Pro	Glu	Leu	Val	Cys	Ser	Met	Leu				
	370					375					380								
His	Leu	Cys	Ser	Gly	Thr	Arg	Leu	Pro	Ala	Leu	Thr	Val	His	Val	Thr				
385					390					395					400				
Gln	Pro	Lys	Asp	Gly	Gly	Phe	Cys	Glu	Val	Cys	Lys	Lys	Leu	Val	Gly				
				405				410						415					
Thr	Leu	Asp	Arg	Asn	Leu	Glu	Lys	Asn	Ser	Thr	Lys	Gln	Glu	Ile	Leu				
			420				425						430						
Ala	Ala	Leu	Glu	Lys	Gly	Cys	Ser	Phe	Leu	Pro	Asp	Pro	Tyr	Gln	Lys				
	435					440					445								
Gln	Cys	Asp	Gln	Phe	Val	Ala	Glu	Tyr	Glu	Pro	Val	Leu	Ile	Glu	Ile				
	450					455					460								
Leu	Val	Glu	Val	Met	Asp	Pro	Ser	Phe	Val	Cys	Leu	Lys	Ile	Gly	Ala				
465					470					475					480				
Cys	Pro	Ser	Ala	His	Lys	Pro	Leu	Leu	Gly	Thr	Glu	Lys	Cys	Ile	Trp				
				485				490						495					
Gly	Pro	Ser	Tyr	Trp	Cys	Gln	Asn	Thr	Glu	Thr	Ala	Ala	Gln	Cys	Asn				
			500				505						510						
Ala	Val	Glu	His	Cys	Lys	Arg	His	Val	Trp	Asn									
	515						520												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
1 5 10 15
Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
20 25 30
Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
35 40 45
Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
50 55 60
Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTACGCCC TCTTCCTCCT GGCCAGCCTC CTGGGCGCGG CTCTAGCCGG CCCGGTCCTT 60
GGACTGAAAG AATGCACCAG GGGCTCGGCA GTGTGGTGCC AGAATGTGAA GACGGCGTCC 120
GACTGCGGGG CAGTGAAGCA CTGCCTGCAG ACCGTTTGGA ACAAGCCAAC AGTGAAATCC 180
CTTCCCTGCG ACATATGCAA AGACGTTGTC ACCGCAGCTG GTGATATGCT GAAGGACAAT 240
GCCACTGAGG AGGAGATCCT TGTTTACTTG GAGAAGACCT GTGACTGGCT TCCGAAACCG 300
AACATGTCTG CTTTCATGCAA GGAGATAGTG GACTCCTACC TCCCTGTCAT CCTGGACATC 360
ATTAAAGGAG AAATGAGCCG TCCTGGGGAG GTGTGCTCTG CTCTCAACCT CTGCGAGTCT 420
CTCCAGAAGC ACCTAGCAGA GCTGAATCAC CAGAAGCAGC TGGAGTCCAA TAAGATCCCA 480
GAGCTGGACA TGACTGAGGT GGTGGCCCCC TTCATGGCCA ACATCCCTCT CCTCCTCTAC 540
CCTCAGGACG GCGCCCGCAG CAAGCCCCAG CCAAAGGATA ATGGGGACGT TTGCCAGGAC 600
TGCATTGAGA TGGTGACTGA CATCCAGACT GCTGTACGGA CCAACTCCAC CTTTGTCCAG 660
GCCTTGGTGG AACATGTCAA GGAGGAGTGT GACCGCCTGG GCCCTGGCAT GGCCGACATA 720
TGCAAGAAGT ATATCAGCCA GTATTCTGAA ATTGCTATCC AGATGATGAT GCACATGCAA 780
CCCAAGGAGA TCTGTGCGCT GGTGCGGTTT TGTGATGAGG TGAAAGAGAT GCCCATGCAG 840
ACTCTGGTCC CCGCCAAAGT GGCCTCCAAG AATGTCATCC CTGCCCTGGA ACTGGTGGAG 900
CCCATTAAAG AGCACGAGGT CCCAGCAAAG TCTGATGTTT ACTGTGAGGT GTGTGAATTC 960
CTGGTGAAGG AGGTGACCAA GCTGATTGAC AACAACAAGA CTGAGAAAGA AATACTCGAC 1020
GCTTTTGACA AAATGTGCTC GAAGCTGCCG AAGTCCCTGT CGGAAGAGTG CCAGGAGGTG 1080
GTGGACACGT ACGGCAGCTC CATCCTGTCC ATCCTGCTGG AGGAGGTCAG CCCTGAGCTG 1140
GTGTGCAGCA TGCTGCACCT CTGCTCTGGC ACGCGGCTGC CTGCACTGAC CGTTCACGTG 1200
ACTCAGCCAA AGGACGGTGG CTTCTGCGAA GTGTGCAAGA AGCTGGTGGG TTATTTGGAT 1260
CGCAACCTGG AGAAAAACAG CACCAAGCAG GAGATCCTGG CTGCTCTTGA GAAAGGCTGC 1320
AGTTTCCTGC CAGACCCTTA CCAGAAGCAG TGTGATCAGT TTGTGGCAGA GTACGAGCCC 1380
GTGCTGATCG AGATCCTGGT GGAGGTGATG GATCCTTCCT TCGTGTGCTT GAAAATTGGA 1440
GCCTGCCCTT CGGCCCATAA GCCCTTGTTG GGAAGTGAAG AGTGTATATG GGGCCCAAGC 1500
TACTGGTGCC AGAACACAGA GACAGCAGCC CAGTGCAATG CTGTGAGCA TTGCAAACGC 1560
CATGTGTGGA ACTAGGAGGA GGAATATTCC ATCTTGGCAG AAACCACAGC ATTGGTTTTT 1620

TTCTACTTGT	GTGTCTGGGG	GAATGAACGC	ACAGATCTGT	TTGACTTTGT	TATAAAAATA	1680
GGGCTCCCCC	ACCTCCCCCA	TTTCTGTGTC	CTTTATTGTA	GCATTGCTGT	CTGCAAGGGA	1740
GGCCCTAGCC	CCTGGCAGAC	ATAGCTGCTT	CAGTGCCCCT	TTTCTCTCTG	CTAGATGGAT	1800
GTTGATGCAC	TGGAGGTCTT	TTAGCCTGCC	CTTGCATGGC	GCCTGCTGGA	GGAGGAGAGA	1860
GCTCTGCTGG	CATGAGCCAC	AGTTTCTTGA	CTGGAGGCCA	TCAACCCTCT	TGGTTGAGGC	1920
CTTGTTCTGA	GCCCTGACAT	GTGCTTGGGC	ACTGGTGGGC	CTGGGCTTCT	GAGGTGGCCT	1980
CCTGCCCTGA	TCAGGGACCC	TCCCCGCTTT	CCTGGGCCTC	TCAGTTGAAC	AAAGCAGCAA	2040
AACAAAGGCA	GTTTTATATG	AAAGATTAGA	AGCCTGGAAT	AATCAGGCTT	TTTAAATGAT	2100
GTAATTCCCA	CTGTAATAGC	ATAGGGATTT	TGGAAGCAGC	TGCTGGTGGC	TTGGGACATC	2160
AGTGGGGCCA	AGGGTTCTCT	GTCCTTGTTT	CAACTGTGAT	TTGGCTTTCC	CGTGTCTTTC	2220
CTGGTGATGC	CTTGTTTGGG	GTTCTGTGGG	TTTGGGTGGG	AAGAGGGCAA	TCTGCCTGAA	2280
TGTAACCTGC	TAGCTCTCCG	AAGGCCCTGC	GGGCCTGGCT	TGTGTGAGCG	TGTGGACAGT	2340
GGTGGCCGCG	CTGTGCCTGC	TCGTGTTGCC	TACATGTCCC	TGGCTGTTGA	GGCGCTGCTT	2400
CAGCCTGCAC	CCCTCCCTTG	TCTCATAGAT	GCTCCTTTTG	ACCTTTTCAA	ATAAATATGG	2460
ATGGCGAGCT	CCTAGGCCTC	TGGCTTCCTG	GTAGAGGGCG	GCATGCCGAA	GGGTCTGCTG	2520
GGTGTGGATT	GGATGCTGGG	GTGTGGGGGT	TGGAAGCTGT	CTGTGGCCCA	CTTGGGCACC	2580
CACGCTTCTG	TCCACTTCTG	GTTGCCAGGA	GACAGCAAGC	AAAGCCAGCA	GGACATGAAG	2640
TTGCTATTAA	ATGGACTTCG	TGATTTTGTG	TTTGCATAAA	AGTTTCTGTG	ATTTAACAAT	2700
AAAATTCTGT	TAGCCAGAAA	AAAAAAAAAA	AAAAAAAAAA			2740

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Lys	Glu	Val	Thr	Lys	Leu	Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu
1				5				10					15		
Ile	Leu														

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Gln	Phe	Val	Met	Asn	Lys	Phe	Ser	Glu	Leu	Ile	Val	Asn	Asn	Ala
1				5				10					15		

Thr Glu Glu Leu Leu Tyr
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Gln Leu Val Asn Arg Lys Leu Ser Glu Leu Ile Ile Asn Asn Ala
1 5 10 15
Thr Glu Glu Leu Leu
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Glu Tyr Val Val Lys Lys Val Met Leu Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Lys Ile Ile
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Glu Phe Val Val Lys Glu Val Ala Lys Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Glu Ile Leu

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 21...21
- (D) OTHER INFORMATION: Xaa=I or L

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Leu Ile Xaa Asn Asn Xaa
 1 5 10 15
 Thr Glu Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn Ala
 1 5 10 15
 Thr Glu Glu Glu Ile Leu
 20